[P3] *In Silico* Design of Inhibitors as Potential Therapeutics for Multiple Myeloma and Leukemias

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According to the Leukemia & Lymphoma Society, in the US approximately every 10 minutes someone dies from a blood cancer. This accounts for 9.4% of the deaths from cancer, out of 580,000 total in 2013. Therefore, there is an urgent need to design and develop new therapies to treat such blood cancers. In order to more rapidly identify drug treatments for blood cancers, new methods that increase the efficiency of the drug discovery process are urgently needed. Toward that end, computational methods have become very instrumental in predicting the binding modes of inhibitors and guiding structure-based design of analogs with improved potency, selectivity, physico-chemical and ADMET properties. In this presentation, the role of computational techniques that helped guide synthetic efforts to develop more potent analogs of G-protein coupled receptor kinase 6 (GRK6) for the treatment of multiple myeloma (MM), and WD repeat-containing protein 5 (WDR5) for the treatment of the MLL-dependent leukemias will be discussed. These targets represent two distinct classes of proteins, namely kinases, and WD repeat family proteins. The comparison and contrast between the computational approaches used to predict the binding modes and understand mechanisms of action of potent ligands for these three targets will be described, as well as how this knowledge could be used to further optimize inhibitors of these targets.